SEQUENCE LISTING

- (1) GENERAL INFORMATION
 - (i) APPLICANT: Hadlaczky, Gyula Szalay, Aladar
- (ii) TITLE OF THE INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
 - (iii) NUMBER OF SEQUENCES: 34
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Heller Ehrman White & McAuliffe
 - (B) STREET: 4350 La Jolla Village Drive, 6th Floor
 - (C) CITY: San Diego
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 92122
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible (C) OPERATING SYSTEM: DOS

 - (D) SOFTWARE: FastSEQ Version 1.5
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:(B) FILING DATE:
 - (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/835,682
 (B) FILING DATE: 10-APR-1997

 - (C) CLASSIFICATION:
 - (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/695,191 (B) FILING DATE: 07-AUG-1996

 - (C) CLASSIFICATION:
 - (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/682,080
 - (B) FILING DATE: 15-JUL-1996
 - (C) CLASSIFICATION:
 - (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/629,822
 - (B) FILING DATE: 10-APR-1996
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Seidman, Stephanie L
 - (B) REGISTRATION NUMBER: 33,779
 - (C) REFERENCE/DOCKET NUMBER: 24601-4021
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 858-450-8403
 - (B) TELEFAX: 858-587-5360
 - (C) TELEX:
 - (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEOUENCE CHARACTERISTICS:
 - (A) LENGTH: 1293 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:
 (ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

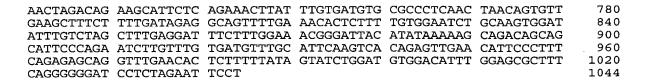
GAATTCATCA	TTTTTCANGT	CCTCAAGTGG	ATGTTTCTCA	TTTNCCATGA	TTTTAAGTTT	60
TCTCGCCATA	TTCCTGGTCC	TACAGTGTGC	ATTTCTCCAT	TTTNCACGTT	TTNCAGTGAT	120
TTCGTCATTT	TCAAGTCCTC	AAGTGGATGT	TTCTCATTTN	CCATGAATTT	CAGTTTTCTN	180
GCCATATTCC	ACGTCCTACA	GNGGACATTT	CTAAATTTNC	CACCTTTTTC	AGTTTTCCTC	240
GCCATATTTC	ACGTCCTAAA	ATGTGTATTT	CTCGTTTNCC	GTGATTTTCA	GTTTTCTCGC	300
CAGATTCCAG	GTCCTATAAT	GTGCATTTCT	CATTTNNCAC	GTTTTTCAGT	GATTTCGTCA	360
TTTTTTCAAG	TCGGCAAGTG	GATGTTTCTC	ATTTNCCATG	ATTTNCAGTT	TTCTTGNAAT	420
ATTCCATGTC	CTACAATGAT	CATTTTTAAT	TTTCCACCTT	TTCATTTTTC	CACGCCATAT	480
TTCATGTCCT	AAAGTGTATA	TTTCTCCTTT	TCCGCGATTT	TCAGTTTTCT	CGCCATATTC	540
CAGGTCCTAC	AGTGTGCATT	CCTCATTTTT	CACCTTTTTC	ACTGATTTCG	TCATTTTTCA	600
AGTCGTCAAC	TGGATCTTTC	TAATTTTCCA	TGATTTTCAG	TTATCTTGTC	ATATTCCATG	660
TCCTACAGTG	GACATTTCTA	AATTTTCCAA	CTTTTTCAAT	TTTTCTCGAC	ATATTTGACG	720
TGCTAAAGTG	TGTATTTCTT	ATTTTCCGTG	ATTTTCAGTT	TTCTCGCCAT	ATTCCAGGTC	780
CTAATAGTGT	GCATTTCTCA	TTTTTCACGT	TTTTCAGTGA	TTTCGTCATT	TTTTCCAGTT	840
GTCAAGGGGA	TGTTTCTCAT	TTTCCATGAG	TGTCAGTTTT	CTTGCTATAT	TCCATGTCCT	900
ACAGTGACAT	TTCTAAATAT	TATACCTTTT	TCAGTTTTTC	TCACCATATT	TCACGTCCTA	960
AAGTATATAT	TTCTCATTTT	CCCTGATTTT	CAGTTTCCTT	GCCATATTCC	AGGTCCTACA	1020
GTGTGCATTT	CTCATTTTTC	ACGTTTTTCA	GTAATTTCTT	CATTTTTTAA	GCCCTCAAAT	1080
GGATGTTTCT	CATTTTCCAT	GATTTTCAGT	TTTCTTGCCA	TATACCATGT	CCTACAGTGG	1140
ACATTTCTAA	ATTATCCACC	TTTTTCAGTT	TTTCATCGGC	ACATTTCACG	TCCTAAAGTG	1200
TGTATTTCTA	ATTTTCAGTG	ATTTTCAGTT	TTCTCGCCAT	ATTCCAGGAC	CTACAGTGTG	1260
CATTTCTCAT	TTTTCACGTT	TTTCAGTGAA	TTC			1293

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1044 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGAAAAAGGA	AATATCTTCC	CCTGAAAACT	AGACAGAAGG	ATTCTCAGAA	60
GATGTGCGCC	CCTCAACTAA	CAGTGTTGAA	GCTTTCTTTT	GATAGAGCAG	120
CTCTTTTTGT	AAAATCTGCA	AGAGGATATT	TGGATAGCTT	TGAGGATTTC	180
GGGATTGTCT	TCATATAAAC	CCTAGACAGA	AGCATTCTCA	GAAGCTTCAT	240
CAGTTGAAGT	CACAGTGTTG	AACAGTCCCC	TTTCATAGAG	CAGGTTTGAA	300
TTGTAGTATC	TGGAAGTGGA	CATTTGGAGC	GATCTCAGGA	CTGCGGTGAA	360
TCTTCCAATA	AAAGCTAGAT	AGAGGCAATG	TCAGAAACCT	TTTTCATGAT	420
AGCTAACAGA	GTTGAACCTT	CCTTTGAGAG	AGCAGTTTTG	AAACACTCTT	480
CTGCAAGTGG	ATATTTGTCT	AGCTTTGAGG	ATTTCGTTGG	GAAACGGGAT	540
AAGCAGACAG	CAGCATTCCC	AGAAACTTCT	TTGTGATGTT	TGCATTCAAG	600
GAACATTCCC	TTTCATAGAG	CAGGTTTGAA	ACACACTTTT	TGATGTATCT	660
ATTTGCAGCG	CTTTCAGGCC	TAAGGTGAAA	AGGAAATATC	TTCCCCTGAA	720
	GATGTGCGCC CTCTTTTTGT GGGATTGTCT CAGTTGAAGT TTGTAGTATC TCTTCCAATA AGCTAACAGA CTGCAAGTGG AAGCAGACAG GAACATTCCC	GATGTGCGCC CCTCAACTAA CTCTTTTTGT AAAATCTGCA GGGATTGTCT TCATATAAAC CAGTTGAAGT CACAGTGTTG TTGTAGTATC TGGAAGTGGA TCTTCCAATA AAAGCTAGAT AGCTAACAGA GTTGAACCTT CTGCAAGTGG ATATTTGTCT AAGCAGACAG CAGCATTCCC GAACATTCCC TTTCATAGAG	GATGTGCGCC CCTCAACTAA CAGTGTTGAA CTCTTTTTGT AAAATCTGCA AGAGGATATT GGGATTGTCT TCATATAAAC CCTAGACAGA CAGTTGAAGT CACAGTGTTG AACAGTCCCC TTGTAGTATC TGGAAGTGGA CATTTGGAGC TCTTCCAATA AAAGCTAGAT AGAGGCAATG AGCTAACAGA GTTGAACCTT CCTTTGAGAG CTGCAAGTGG ATATTTGTCT AGCTTTGAGG AAGCAGACAG CAGCATTCCC AGAAACTTCT GAACATTCCC TTTCATAGAG CAGGTTTGAA	GATGTGCGCC CCTCAACTAA CAGTGTTGAA GCTTTCTTT CTCTTTTTGT AAAATCTGCA AGAGGATATT TGGATAGCTT GGGATTGTCT TCATATAAAC CCTAGACAGA AGCATTCTCA CAGTTGAAGT CACAGTGTTG AACAGTCCCC TTTCATAGAG TTGTAGTATC TGGAAGTGGA CATTTGGAGC GATCTCAGGA TCTTCCAATA AAAGCTAGAT AGAGGCAATG TCAGAAACCT AGCTAACAGA GTTGAACCTT CCTTTGAGAG AGCAGTTTTG CTGCAAGTGG ATATTTGTCT AGCTTTGAGG ATTTCGTTGG AAGCAGACAG CAGCATTCCC AGAAACTTCT TTGTGATGTT GAACATTCCC TTTCATAGAG CAGGTTTGAA ACACACTTTT	TGAAAAAGGA AATATCTTCC CCTGAAAACT AGACAGAAGG ATTCTCAGAA GATGTGCGCC CCTCAACTAA CAGTGTTGAA GCTTTCTTTT GATAGAGCAG CTCTTTTTGT AAAATCTGCA AGAGGATATT TGGATAGCTT TGAGGATTCC GGGATTGTCT TCATATAAAC CCTAGACAGA AGCATTCTCA GAAGCTTCAT CAGTTGAAGT CACAGTGTTG AACAGTCCCC TTTCATAGAG CAGGTTTGAA TTGTAGTATC TGGAAGTGGA CATTTGGAGC GATCTCAGGA CTGCCGTGAA TCTTCCAATA AAAGCTAGAT AGAGGCAATG TCAGAAACCT TTTTCATGAT AGCTAACAGA GTTGAACCTT CCTTTGAGAG AGCAGTTTTG AAACACTCTT CTGCAAGTGG ATATTTGTCT AGCTTTGAGG ATTTCGTTGG GAAACGGGAT AAGCAGACAG CAGCATTCCC AGAAACTTCT TTGTGATGTT TGCATTCAAG GAACATTCCC TTTCATAGAG CAGGTTTGAA ACACACTTTT TGATGTATCT ATTTGCAGCG CTTTCAGGCC TAAGGTGAAA AGGAAATATC TTCCCCTGAA



(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGCAGCTGG	GGGTCTCCAA	TCAGGCAGGG	GCCCCTTACT	ACTCAGATGG	GGTGGCCGAG	60
TAGGGGAAGG	GGGTGCAGGC	TGCATGAGTG	GACACAGCTG	TAGGACTACC	TGGGGGCTGT	120
GGATCTATGG	GGGTGGGGAG	AAGCCCAGTG	ACAGTGCCTA	GAAGAGACAA	GGTGGCCTGA	180
GAGGGTCTGA	GGAACATAGA	GCTGGCCATG	TTGGGGCCAG	GTCTCAAGCA	GGAAGTGAGG	240
AATGGGACAG	GCTTGAGGAT	ACTCTACTCA	GTAGCCAGGA	TAGCAAGGAG	GGCTTGGGGT	300
TGCTATCCTG	GGGTTCAACC	CCCCAGGTTG	AAGGCCCTGG	GGGAGATGGT	CCCAGGACAT	360
ATTACAATGG	ACACAGGAGG	TTGGGACACC	TGGAGTCACC	AAACAAAACC	ATGCCAAGAG	420
AGACCATGAG	TAGGGGTGTC	CAGTCCAGCC	CTCTGACTGA	GCTGCATTGT	TCAAATCCAA	480
AGGGCCCCTG	CTGCCACCTA	GTGGCTGATG	GCATCCACAT	GACCCTGGGC	CACACGCGTT	540
TAGGGTCTCT	GTGAAGACCA	AGATCCTTGT	TACATTGAAC	GACTCCTAAA	TGAGCAGAGA	600
TTTCCACCTA	TTCGAAACAA	TCACATAAAA	TCCATCCTGG	AAAAAGCCTG	GGGGATGGCA	660
CTAAGGCTAG	GGATAGGGTG	GGATGAAGAT	TATAGTTACA	GTAAGGGGTT	TAGGGTTAGG	720
GATCAACGTT	GGTTAGGAGT	TAGGGATACA	GTAGGGTACC	GGTAGGGTTA	GGGGTTAGGG	780
TTAGGGGTTA	GGGTTAGGGT	TAGGGTTAGG	GTTAGGGTTA	GGGGTTAGGG	GTTAGGGTTA	840
GGGTTAGGTT	TTGGGGTGGC	GTATTTTGGT	CTTATACGCT	GTGTTCCACT	GGCAATGAAA	900
AGAGTTCTTG	TTTTTCCTTC	AGCAATTTGT	CATTTTTAAA	AGAGTTTAGC	AATTCTAACA	960
GATATAGACC	AGCTGTGCTA	TCTCATTGTG	GTTTTCAATT	GTAACCACAT	TGTGGTTTCA	1020
ATGTGTTTAC	TTGCCATCTG	TAGATCTTCT	TTGCGTGAGG	TGTCTGTTCA	GATGTGTGTG	1080
CATTTCTTGN	NTTTNGGCTG	TTTAACTTAT	TGTTTAGTTT	TAATAATTTT	TTATATATTT	1140
GAAGACAAAT	CTTTCTCAGA	TGTGTATTTG	CAAATATTTC	TTCAATATGA	GGCTTGCTTT	1200
TGTCTCTAAC	AAGGTCTCTT	CAGAGATAAC	TTAAATATAA	GAAATCCACA	CTGTCACTTC	1260
TTTTGTGTAT	ATCTACCTTT	TGTGTCATTT	GTTAAAATTC	ATTACCAAAC	CCAAAGGCAG	1320
ATAGCTTTTC	TTCTATTGTT	TCTTCTAGAA	ATTTGTATAG	TTTTGCATTT	TTAGTGTAAG	1380
GATGATTTTG	AGTGATTATT	TGTGTAAGTT	GTAAAGTTTT	CGTCTATATC	CATATCATTT	1440
CTTATGGTTT	CCAATTAATC	GTTCCCTCAC	TATTTTTGGG	AAAGACACAG	GATAGTGGGC	1500
TTTGTTAGAG	TAGATAGGTA	GCTAGACATG	AACAGGAGGG	GGCCTCCTGG	AAAAGGGAAA	1560
GTCTGGGAAG	GCTCACCTGG	AGGACCACCA	AAAATTCACA	TATTAGTAGC	ATCTCTAGTG	1620
CTGGAGTGGA	TGGGCACTTG	TCAATTGTGG	GTAGGAGGGA	AAAGAGGTCC	TATGCAGAAA	1680
GAAACTCCCT	AGAACTCCTC	TGAAGATGCC	CCAATCATTC	ACTCTGCAAT	AAAAATGTCA	1740
GAATATTGCT	AGCTACATGC	TGATAAGGNN	AAAGGGGACA	TTCTTAAGTG	AAACCTGGCA	1800
CCATAAGTAC	AGATTAGGGC	AGAGAAGGAC	ATTCAAAAGA	GGCAGGCGCA	GTAGGTACAA	1860
ACGTGATCGC	TGTCAGTGTG	CCTGGGATGG	CGGGAAGGAG	GCTGGTGCCA	GAGTGGATTC	1920
GTATTGATCA	CCACACATAT	ACCTCAACCA	ACAGTGAGGA	GGTCCCACAA	GCCTAAGTGG	1980
GGCAAGTTGG	GGAGCTAAGG	CAGTAGCAGG	AAAACCAGAC	AAAGAAAACA	GGTGGAGACT	2040
TGAGACAGAG	GCAGGAATGT	GAAGAAATCC	AAAATAAAAT	TCCCTGCACA	GGACTCTTAG	2100
GCTGTTTAAT	GCATCGCTCA	GTCCCACTCC	TCCCTATTTT	TCTACAATAA	ACTCTTTACA	2160
CTGTGTTTCT	TTTCAATGAA	GTTATCTGCC	ATCTTTGTAT	TGCCTCTTGG	TGAAAATGTT	2220
TCTTCCAAGT	TAAACAAGAA	CTGGGACATC	AGCTCTCCCC	AGTAATAGCT	CCGTTTCAGT	2280
TTGAATTTAC	AGAACTGATG	GGCTTAATAA	CTGGCGCTCT	GACTTTAGTG	GTGCAGGAGG	2340

CCTCGACACT GACAGCAATA GGGTCCGGCA GTGTCCCCAG CTGCCAGCAG GGGGCGTACG	2400 2460 2492
(2) INFORMATION FOR SEQ ID NO:4:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: Genomic DNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE: (ix) FEATURE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
GGGGAATTCA TTGGGATGTT TCAGTTGA	28
(2) INFORMATION FOR SEQ ID NO:5:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 29 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: Genomic DNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE: (ix) FEATURE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
CGAAAGTCCC CCCTAGGAGA TCTTAAGGA	29
(2) INFORMATION FOR SEQ ID NO:6:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 47 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: RNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE: (ix) FEATURE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	

(2) INFORMATION FOR SEQ ID NO:7:

CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC



	24601-4
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: Genomic DNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE: (ix) FEATURE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
CGATTTAAAT TAATTAAGCC CGGGC	25
(2) INFORMATION FOR SEQ ID NO:8:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 27 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: Genomic DNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE: (ix) FEATURE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
TAAATTTAAT TAATTCGGGC CCGTCGA	27
(2) INFORMATION FOR SEQ ID NO:9:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 69 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA(D) OTHER INFORMATION IL-2 signal sequence	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu	48

- (ii) MOL
 - (D) O
- (xi) SEQ

ATG TAC AGG AT Met Tyr Arg Me

GTC ACA AAC AGT GCA CCT ACT Val Thr Asn Ser Ala Pro Thr

69

- (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 945 base pairs
 (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

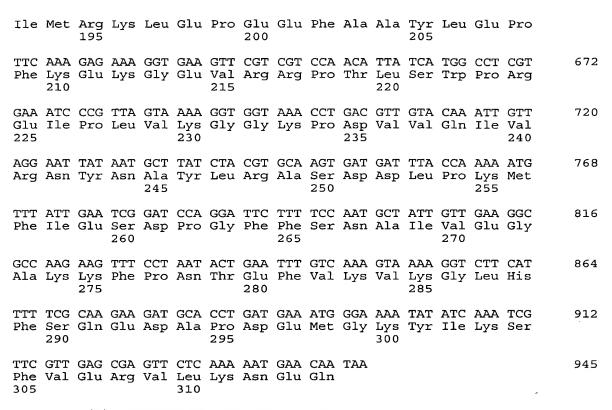
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence

 - (B) LOCATION: 1...942
 (D) OTHER INFORMATION: Renilla Reinformis Luciferase
- (x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

					TCG Ser											48
					CAG Gln											96
					AAT Asn											144
					CAT His											192
	_				ATT Ile 70											240
					AAA Lys											288
					AAA Lys											336
					TTT Phe											384
					TAT Tyr											432
					GTA Val 150											480
					ATT Ile											528
					AAC Asn											576
ATC	ATG	AGA	AAG	TTA	GAA	CCA	GAA	GAA	TTT	GCA	GCA	TAT	CTT	GAA	CCA	624



- (2) INFORMATION FOR SEQ ID NO:11:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTGAATTC A TGTACAGGAT GCAACTCCTG

30

- (2) INFORMATION FOR SEQ ID NO:12:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGAATTCA GTAGGTGCAC TGTTTGTCAC

30

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1434 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	AGAGCAGCGT	TGGGGGATAA	60
TGTCGACATT	TCCACTCCCA	ATGACGGTGA	TGTATAATGC	TCAAGTATTC	TCCTGCTTTT	120
TTACCACTAA	CTAGGAACTG	GGTTTGGCCT	TAATTCAGAC	AGCCTTGGCT	CTGTCTGGAC	180
AGGTCCAGAC	GACTGACACC	ATTAACACTT	TGTCAGCCTC	AGTGACTACA	GTCATAGATG	240
AACAGGCCTC	AGCTAATGTC	AAGATACAGA	GAGGTCTCAT	GCTGGTTAAT	CAACTCATAG	300
ATCTTGTCCA	GATACAACTA	GATGTATTAT	GACAAATAAC	TCAGCAGGGA	TGTGAACAAA	360
AGTTTCCGGG	ATTGTGTGTT	ATTTCCATTC	AGTATGTTAA	ATTTACTAGG	ACAGCTAATT	420
TGTCAAAAAG	TCTTTTTCAG	TATATGTTAC	AGAATTGGAT	GGCTGAATTT	GAACAGATCC	480
TTCGGGAATT	GAGACTTCAG	GTCAACTCCA	CGCGCTTGGA	CCTGTCGCTG	ACCAAAGGAT	540
TACCCAATTG	GATCTCCTCA	GCATTTTCTT	TCTTTAAAAA	ATGGGTGGGA	TTAATATTAT	600
TTGGAGATAC	ACTTTGCTGT	GGATTAGTGT	TGCTTCTTTG	ATTGGTCTGT	AAGCTTAAGG	660
CCCAAACTAG	GAGAGACAAG	GTGGTTATTG	CCCAGGCGCT	TGCAGGACTA	GAACATGGAG	720
CTTCCCCTGA	TATATGGTTA	TCTATGCTTA	GGCAATAGGT	CGCTGGCCAC	TCAGCTCTTA	780
TATCCCACGA	GGCTAGTCTC	ATTGTACGGG	ATAGAGTGAG	TGTGCTTCAG	CAGCCCGAGA	840
GAGTTGCAAG	GCTAAGCACT	GCAATGGAAA	GGCTCTGCGG	CATATATGTG	CCTATTCTAG	900
GGGGACATGT	CATCTTTCAT	GAAGGTTCAG	TGTCCTAGTT	CCCTTCCCCC	AGGCAAAACG	960
ACACGGGAGC	AGGTCAGGGT	TGCTCTGGGT	AAAAGCCTGT	GAGCCTGGGA	GCTAATCCTG	1020
TACATGGCTC	CTTTACCTAC	ACACTGGGGA	TTTGACCTCT	ATCTCCACTC	TCATTAATAT	1080
GGGTGGCCTA	TTTGCTCTTA	TTAAAAGGAA	AGGGGGAGAT	GTTGGGAGCC	GCGCCCACAT	1140
TCGCCGTTAC	AAGATGGCGC	TGACAGCTGT	GTTCTAAGTG	GTAAACAAAT	AATCTGCGCA	1200
TGTGCCGAGG	GTGGTTCTTC	ACTCCATGTG	CTCTGCCTTC	CCCGTGACGT	CAACTCGGCC	1260
GATGGGCTGC	AGCCAATCAG	GGAGTGACAC	GTCCTAGGCG	AAGGAGAATT	CTCCTTAATA	1320
GGGACGGGGT	TTCGTTCTCT	CTCTCTCTCT	TGCTTCTCTC	TCTTGCTTTT	TCGCTCTCTT	1380
GCTTCCCGTA	AAGTGATAAT	GATTATCATC	TACATATCAC	AACGTGCGTG	GAGG	1434

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	AGAGCAGCGT	TGGGGGATAA	60
TGTCGACATT	TCCACTCCCA	ATGACGGTGA	TGTATAATGC	TCAAGTATTC	TCCTGCTTTT	120
TTACCACTAA	CTAGGAACTG	GGTTTGGCCT	TAATTCAGAC	AGCCTTGGCT	CTGTCTGGAC	180
AGGTCCAGAT	ACAACTAGAT	GTATTATGAC	AAATAACTCA	GCAGGGATGT	GAACAAAAGT	240

TTCCGGGATT	GCGTGTTATT	TCCATCCAGT	ATGTTAAATT	TACTAGGGCA	GCTAATTTGT	300
CAAAAAGTCT	TTTCCAGTAT	ATGTTACAGA	ATTGGATGGC	TGAATTTGAA	CAGATCCTTC	360
GGGAATTGAG	ACTTCAGGTC	AACTCCACGC	GCTTGGACCT	GTCCCTGACC	AAAGGATTAC	420
CCAATTGGAT	CTCCTCAGCA	TTTTCTTTCT	TTAAAAAATG	GGTGGGATTA	ATATTATTTG	480
GAGATACACT	TTGCTGTGGA	TTAGTGTTGC	TTCTTTGATT	GGTCTGTAAG	CTTAAGGCCC	540
AAACTAGGAG	AGACAAGGTG	GTTATTGCCC	AGGCGCTTGC	AGGACTAGAA	CATGGAGCTT	600
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GGTGGTTCTT	CACTCCATGT	GCTCTGCCTT	CCCCGTGACG	TCAACTCGGC	CGATGGGCTG	1140
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(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1369 base pairs

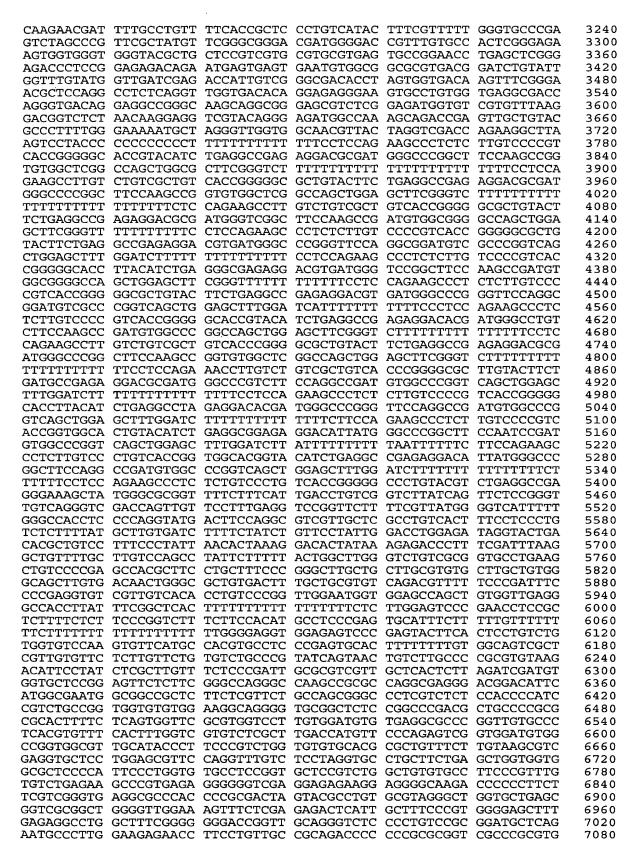
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

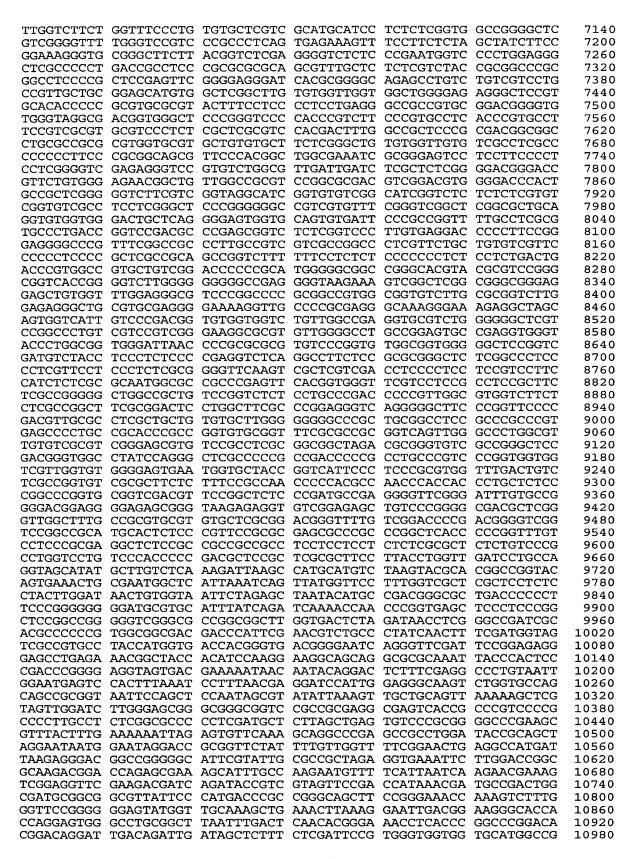
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- (2) INFORMATION FOR SEQ ID NO:16:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22118 base pairs

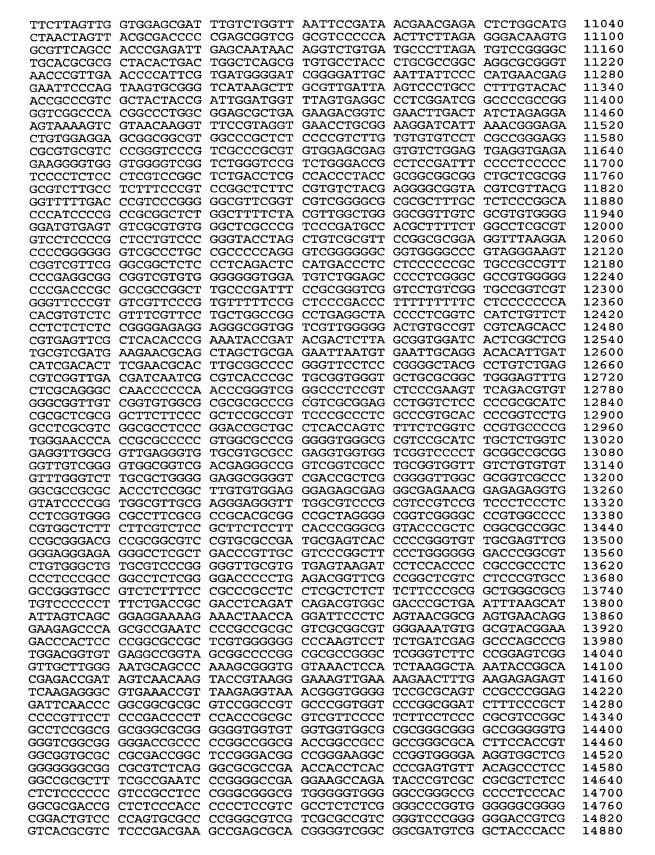
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

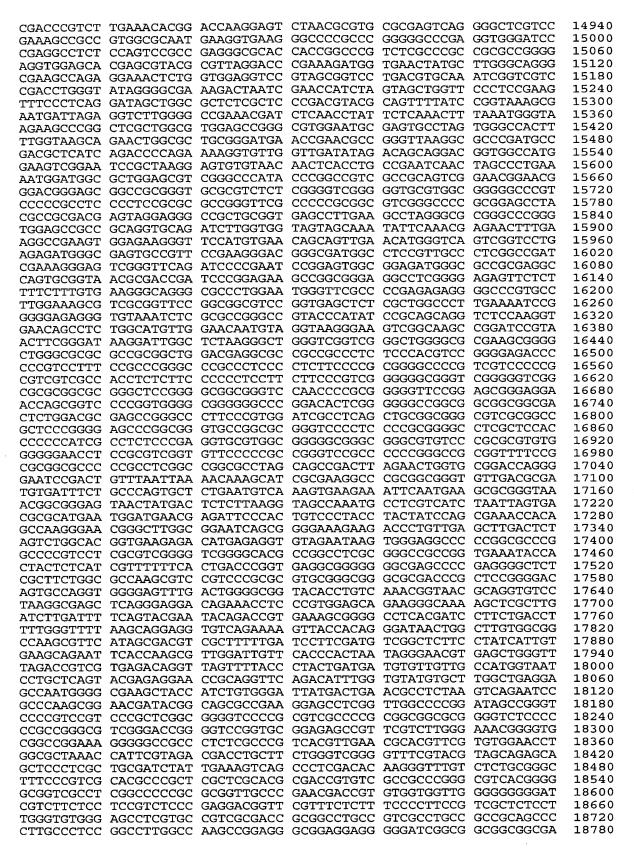
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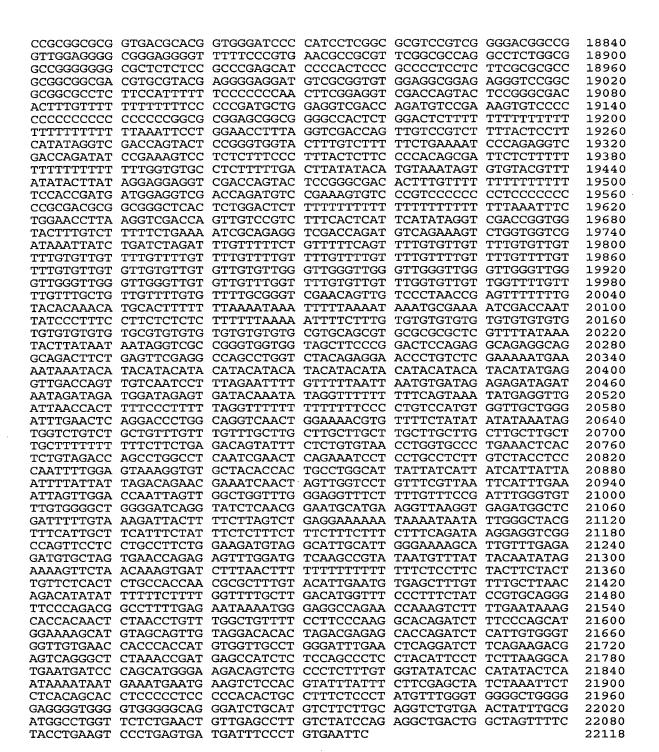












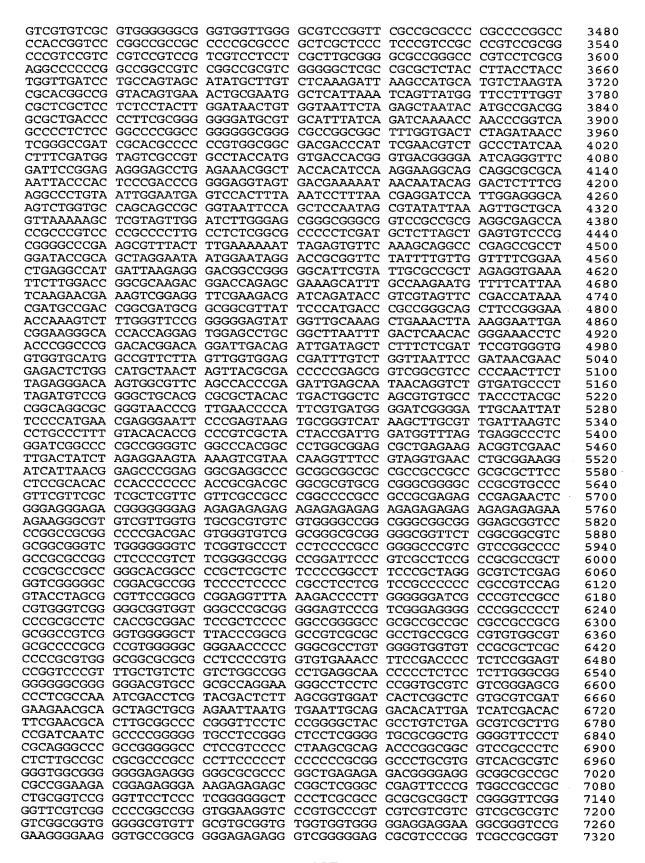
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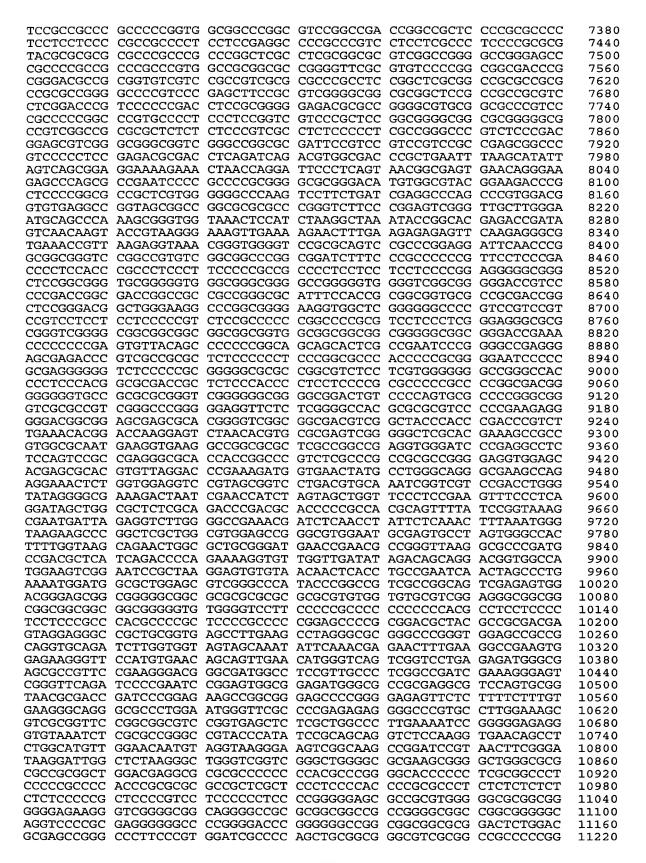
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42999 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:

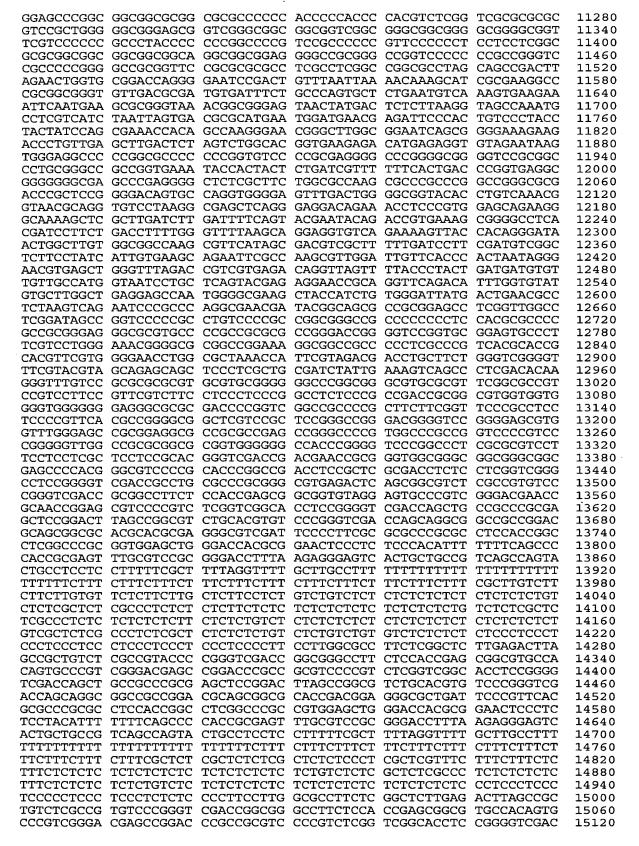
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

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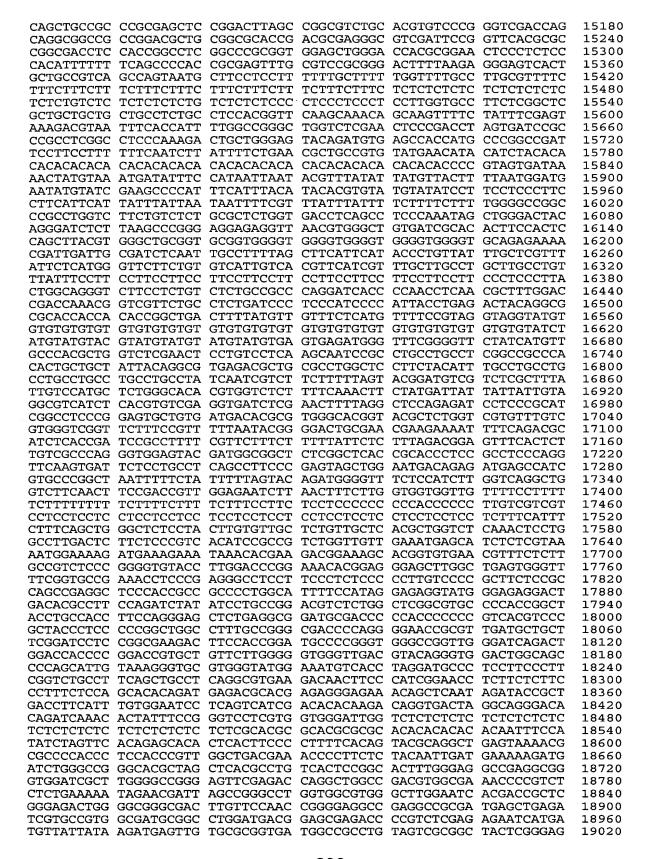


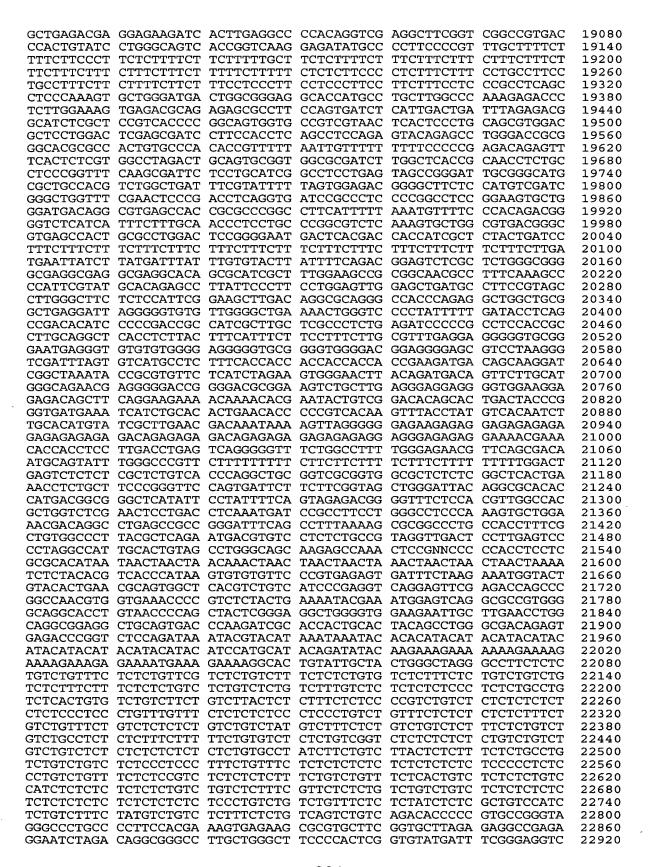


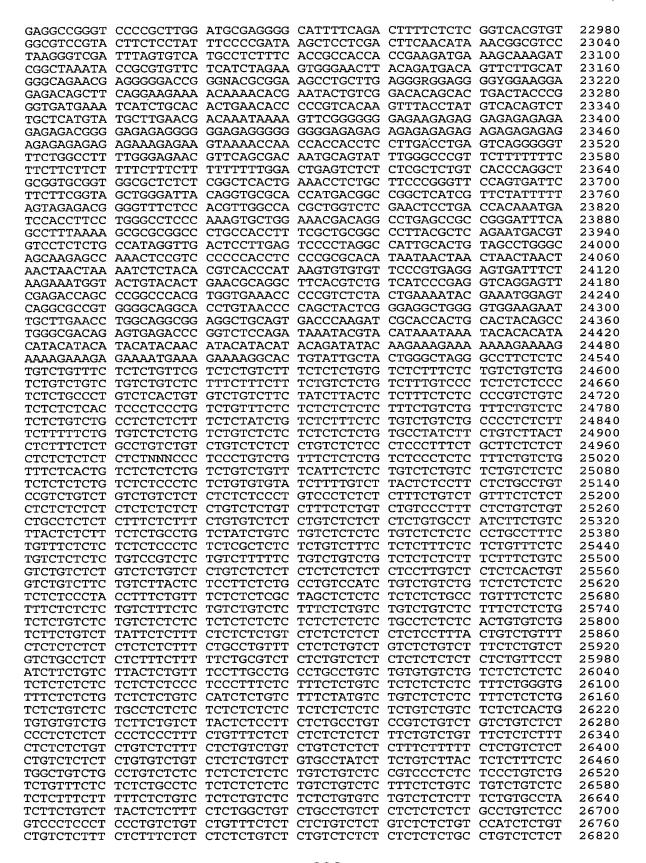




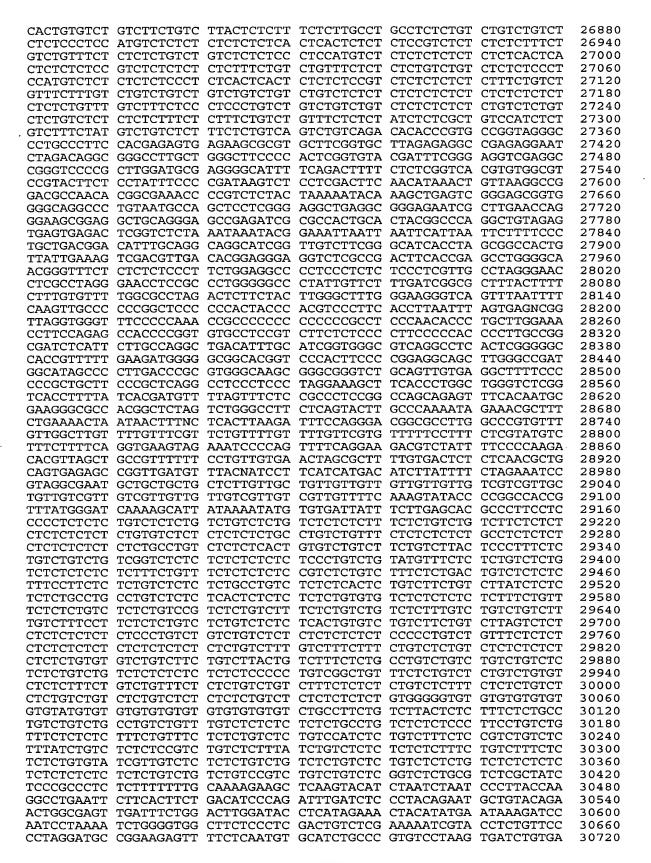










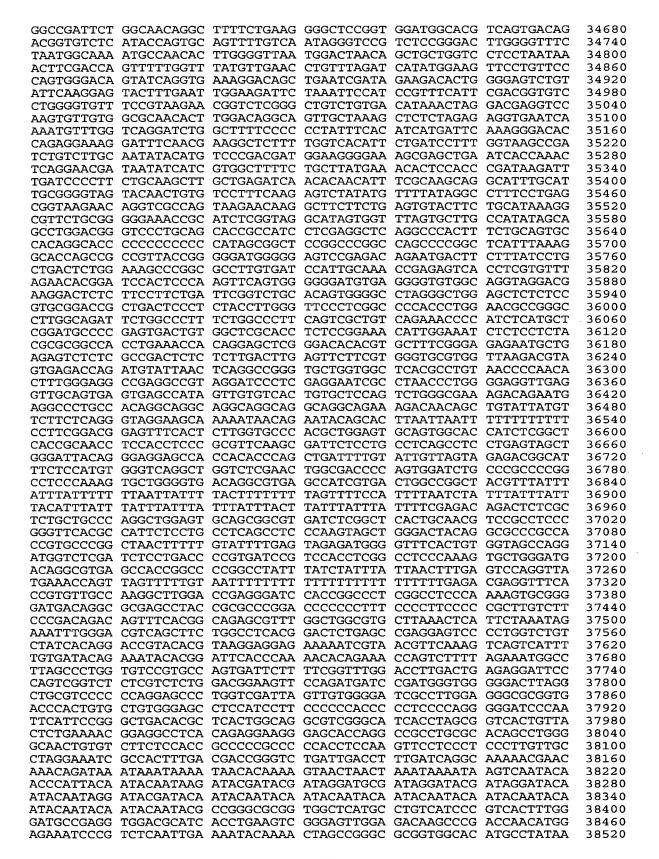


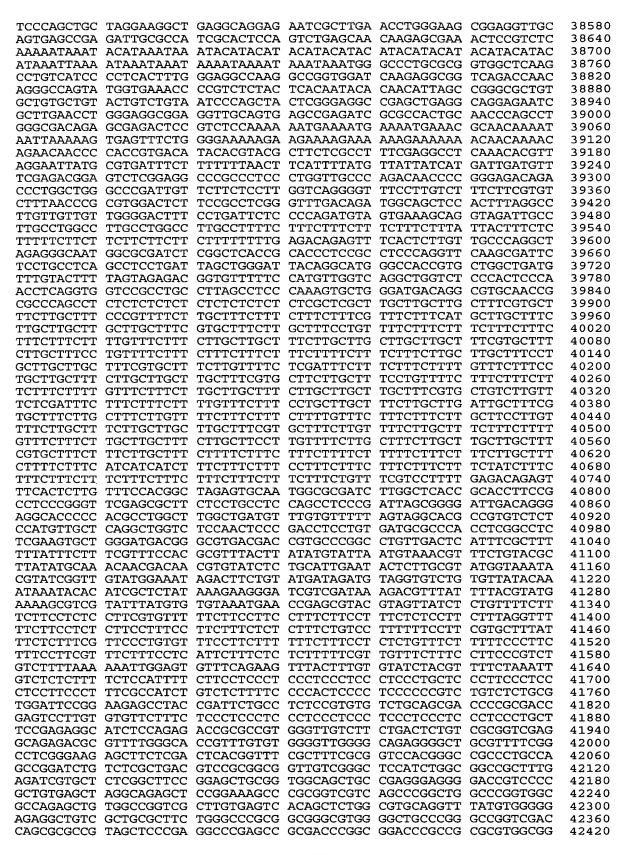




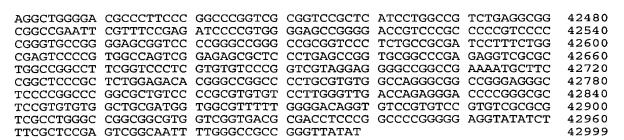
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(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 175 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTCCCGCGCG	GCCCCGTGT	TCGCCGTTCC	CGTGGCGCGG	ACAATGCGGT	TGTGCGTCCA	60
CGTGTGCGTG	TCCGTGCAGT	GCCGTTGTGG	AGTGCCTCGC	TCTCCTCCTC	CTCCCCGGCA	120
GCGTTCCCAC	GGTTGGGGAC	CACCGGTGAC	CTCGCCCTCT	TCGGGCCTGG	ATCCG	175

- (2) INFORMATION FOR SEQ ID NO:19:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 755 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTCTGGTGG	GAATTGTTGA	CCTCGCTCTC	GGGTGCGGCC	TTTGGGGAAC	GGCGGGGTCG	60
GTCGTGCCCG	GCGCCGGACG	TGTGTCGGGG	CCCACTTCCC	GCTCGAGGGT	GGCGGTGGCG	120
GCGGCGTTGG	TAGTCTCCCG	TGTTGCGTCT	TCCCGGGCTC	TTGGGGGGGG	TGCCGTCGTT	180
TTCGGGGCCG	GCGTTGCTTG	GCTTACGCAG	GCTTGGTTTG	GGACTGCCTC	AGGAGTCGTG	240
GGCGGTGTGA	TTCCCGCCGG	TTTTGCCTCG	CGTCTGCCTG	CTTTGCCTCG	GGTTTGCTTG	300
GTTCGTGTCT	CGGGAGCGGT	GGTTTTTTTT	TTTTTCGGGT	CCCGGGGAGA	GGGGTTTTTC	360
CGGGGGACGT	TCCCGTCGCC	'CCCTGCCGCC	GGTGGGTTTT	CGTTTCGGGC	TGTGTTCGTT	420
TCCCCTTCCC	CGTTTCGCCG	TCGGTTCTCC	CCGGTCGGTC	GGCCCTCTCC	CCGGTCGGTC	480
GCCCGGCCGT	GCTGCCGGAC	CCCCCCTTCT	GGGGGGGATG	CCCGGGCACG	CACGCGTCCG	540
GGCGGCCACT	GTGGTCCGGG	AGCTGCTCGG	CAGGCGGGTG	AGCCAGTTGG	AGGGGCGTCA	600
TGCCCCCGCG	GGCTCCCGTG	GCCGACGCGG	CGTGTTCTTT	GGGGGGCCT	GTGCGTGCGG	660
GAAGGCTGCG	CACGTTGTCG	GTCCTTGCGA	GGGAAAGAGG	CTTTTTTTT	TTAGGGGGTC	720
GTCCTTCGTC	GTCCCGTCGG	CGGTGGATCC	GGCCT			755

- (2) INFORMATION FOR SEQ ID NO:20:
- (i) SEQUENCE CHARACTERISTICS:





- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCCGAGGTG	CGTCTGCGGG	TTGGGGCTCG	TCCGGCCCCG	TCGTCCTCCG	GGAAGGCGTT	60
TAGCGGGTAC	CGTCGCCGCG	CCGAGGTGGG	CGCACGTCGG	TGAGATAACC	CCGAGCGTGT	120
TTCTGGTTGT	TGGCGGCGGG	GGCTCCGGTC	GATGTCTTCC	CCTCCCCCTC	TCCCCGAGGC	180
CAGGTCAGCC	TCCGCCTGTG	GGCTTCGTCG	GCCGTCTCCC	CCCCCTCAC	GTCCCTCGCG	240
AGCGAGCCCG	TCCGTTCGAC	CTTCCTTCCG	CCTTCCCCCC	ATCTTTCCGC	GCTCCGTTGG	300
CCCCGGGGTT	TTCACGGCGC	CCCCCACGCT	CCTCCGCCTC	TCCGCCCGTG	GTTTGGACGC	360
CTGGTTCCGG	TCTCCCCGCC	AAACCCCGGT	TGGGTTGGTC	TCCGGCCCCG	GCTTGCTCTT	420
CGGGTCTCCC	AACCCCCGGC	CGGAAGGGTT	CGGGGGTTCC	GGG		463

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGATTCTTCA	GGATTGAAAC	CCAAACCGGT	TCAGTTTCCT	TTCCGGCTCC	GGCCGGGGGG	60
GGCGGCCCCG	GGCGGTTTGG	TGAGTTAGAT	AACCTCGGGC	CGATCGCACG	CCCCCGTGG	120
CGGCGACGAC	CCATTCGAAC	GTCTGCCCTA	TCAACTTTCG	ATGGTAGTCG	ATGTGCCTAC	180
CATGGTGACC	ACGGGTGACG	GGGAATCAGG	GTTCGATTCC	GGAGAGGGAG	CCTGAGAAAC	240
GGCTACCACA	TCCAAGGAAG	GCAGCAGGCG	CGCAAATTAC	CCACTCCCGA	CCCGGGGAGG	300
TAGTGACGAA	AAATAACAAT	ACAGGACTCT	TTCGAGGCCC	TGTAATTGGA	ATGAGTCCAC	360
TTTAAATCCT	TTAAGCAG					378

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATCCATTGG	AGGGCAAGTC	TGGTGCCAGC	AGCCGCGGTA	ATTCCAGCTC	CAATAGCGTA	60
TATTAAAGTT	GCTGCAGTTA	AAAAGCTCGT	AGTTGGATCT	TGGGAGCGGG	CGGGCGGTCC	120
GCCGCGAGGC	GAGTCACCGC	CCGTCCCCGC	CCCTTGCCTC	TCGGCGCCCC	CTCGATGCTC	180





TTAGCTGAGT	TGTCCCGCGG	GGCCCGAAGC	GTTTACTTTG	AAAAAATTAG	AGTTGTTTCA	240
AAGCAGGCCC	GAGCCGCCTG	GATACCGCCA	GCTAGGAAAT	AATGGAATAG	GACCGCGGTT	300
CCTATTTTGT	TTGGTTTTCG	GAACTGAGCC	CATGATTAAG	GGAAACGGCC	GGGGGCATTC	360
CCTTATTGCG	CCCCCTA					378

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 719 base pairs
 (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATCTTTCC	CGCTCCCCGT	TCCTCCCGGC	CCCTCCACCC	GCGCGTCTCC	CCCCTTCTTT	60
TCCCCTCTCC	GGAGGGGGG	GAGGTGGGGG	CGCGTGGGCG	GGGTCGGGGG	TGGGGTCGGC	120
GGGGGACCGC	CCCCGGCCGG	CAAAAGGCCG	CCGCCGGGCG	CACTTCAACC	GTAGCGGTGC	180
GCCGCGACCG	GCTACGAGAC	GGCTGGGAAG	GCCCGACGGG	GAATGTGGCT	CGGGGGGGC	240
GGCGCGTCTC	AGGGCGCCC	GAACCACCTC	ACCCCGAGTG	TTACAGCCCT	CCGGCCGCGC	300
TTTCGCGGAA	TCCCGGGGCC	GAGGGGAAGC	CCGATACCCG	TCGCCGCGCT	TTTCCCCTCC	360
CCCCGTCCGC	CTCCCGGGCG	GGCGTGGGGG	TGGGGGCCGG	GCCGCCCCTC	CCACGCCCGT	420
GGTTTCTCTC	TCTCCCGGTC	TCGGCCGGTT	TGGGGGGGGG	AGCCCGGTTG	GGGGCGGGC	480
GGACTGTCCT	CAGTGCGCCC	CGGGCGTCGT	CGCGCCGTCG	GGCCCGGGGG	GTTCTCTCGG	540
TCACGCCGCC	CCCGACGAAG	CCGAGCGCAC	GGGGTCGGCG	GCGATGTCGG	CTACCCACCC	600
GACCCGTCTT	GAAACACGGA	CCAAGGAGTC	TAACGCGTGC	GCGAGTCAGG	GGCTCGCACG	660
AAAGCCGCCG	TGGCGCAATG	AAGGTGAAGG	GCCCCGTCCG	GGGGCCCGAG	GTGGGATCC	719

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 685 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGAGGCCTCT CCAGTCCGCC	GAGGGCGCAC	CACCGGCCCG	TCTCGCCCGC	CGCGTCGGGG	60
AGGTGGAGCA CGAGCGTACG	CGTTAGGACC	CGAAAGATGG	TGAACTATGC	CTGGGCAGGG	120
CGAAGCCAGA GGAAACTCTG	GTGGAGGTCC	GTAGCGGTCC	TGACGTGCAA	ATCGGTCGTC	180
CGACCTGGGT ATAGGGGCGA	AAGACTAATC	GAACCATCTA	GTAGCTGGTT	CCCTCCGAAG	240
TTTCCCTCAG GATAGCTGGC	GCTCTCGCAA	CCTTCGGAAG	CAGTTTTATC	CGGGTAAAGG	300
CGGAATGGAT TAGGAGGTCT	TGGGGCCGGA	AACGATCTCA	AACTATTTCT	CAAACTTTAA	360
ATGGGTAAGG AAGCCCGGCT	CGCTGGCGTG	GAGCCGGGCG	TGGAATGCGA	GTGCCTAGTG	420
GGCCACTTTT GGTAAGCAGA	ACTGGCGCTG	CGGGATGAAC	CGAACGCCGG	GTTAAGGCGC	480
CCGATGCCGA CGCTCATCAG	ACCCCAGAAA	AGGTGTTGGT	TGATATAGAC	AGCAGGACGG	540
TGGCCATGGA AGTCGGAATC	CGCTAAGGAG	TGTGTAACAA	CTCACCTGCC	GAATCAACTA	600
GCCCTGAAAA TGGATGGCGC	TGGAGCGTCG	GGCCCATACC	CGGCCGTCGC	CGGCAGTCGG	660
AACGGGACGG GACGGGAGCG	GCCGC			•	685

(2) INFORMATION FOR SEQ ID NO:25:



(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
<pre>(ii) MOLECULE TYPE: Genomic DNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
GAGGAATTCC CCTATCCCTA ATCCAGATTG GTG
(2) INFORMATION FOR SEQ ID NO:26:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 35 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
<pre>(ii) MOLECULE TYPE: Genomic DNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
AAACTGCAGG CCGAGCCACC TCTCTTCTGT GTTTG 35
(2) INFORMATION FOR SEQ ID NO:27:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
<pre>(ii) MOLECULE TYPE: Genomic DNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
AGGAATTCAC AGAAGAGAG TGGCTCGGCC TGC 33
(2) INFORMATION FOR SEQ ID NO:28:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 34 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: Genomic DNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
AGCCTGCAGG AAGTCATACC TGGGGAGGTG GCCC	34
(2) INFORMATION FOR SEQ ID NO:29:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 80 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: Genomic DNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
AAACTGCAGG TTAATTAACC CTAACCCTAA CCCTAACCCT AACCCTAACC CTAACCCTAA CCCTAACCCT AACCCGGGAT	60 80
(2) INFORMATION FOR SEQ ID NO:30:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 19 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: Genomic DNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
TTGGGCCCTA GGCTTAAGG	19
(2) INFORMATION FOR SEQ ID NO:31:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCAGGGTTT TCCCAGTCAC GACGT

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

26

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(D) TOPOLOGY: linear (ii) MOLECULE TYPE: Genomic DNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
GCTGCAAGGC GATTAAGTTG GGTAAC
(2) INFORMATION FOR SEQ ID NO:33:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 26 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: Genomic DNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
TATGTTGTGT GGAATTGTGA GCGGAT
(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGTTTAAAC AGATCTCTGC A

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